

FIG. 1A

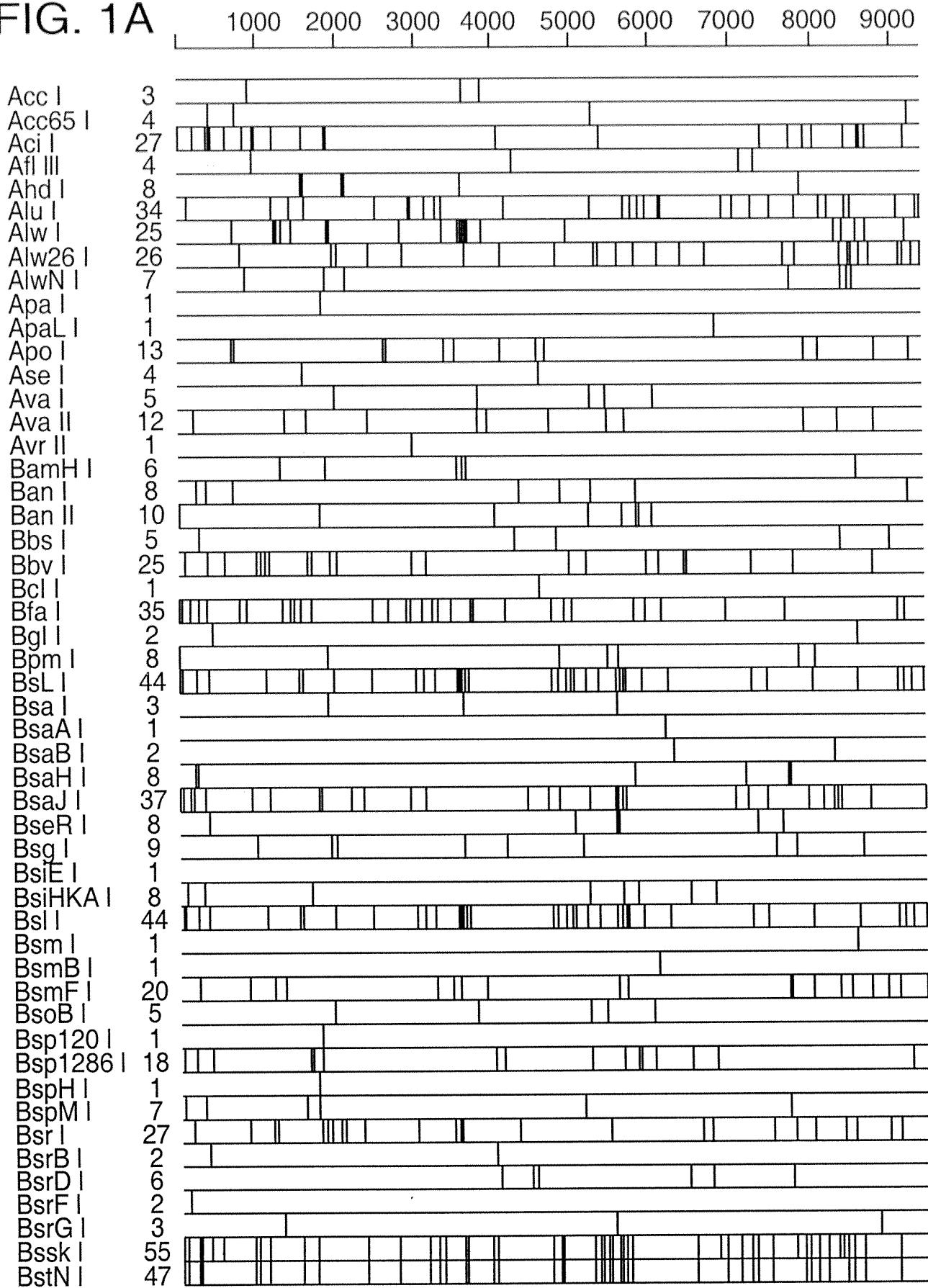


FIG. 1B

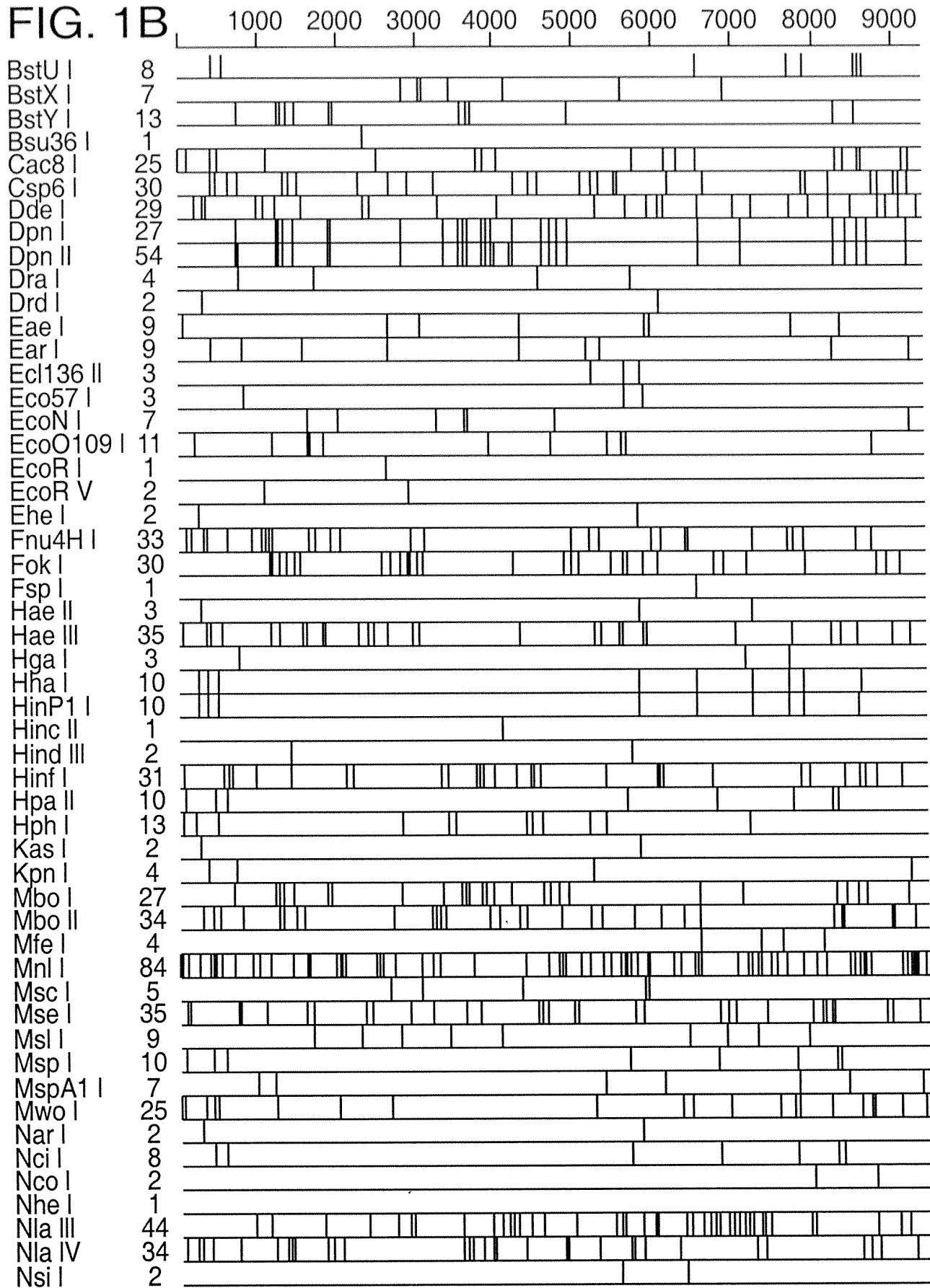
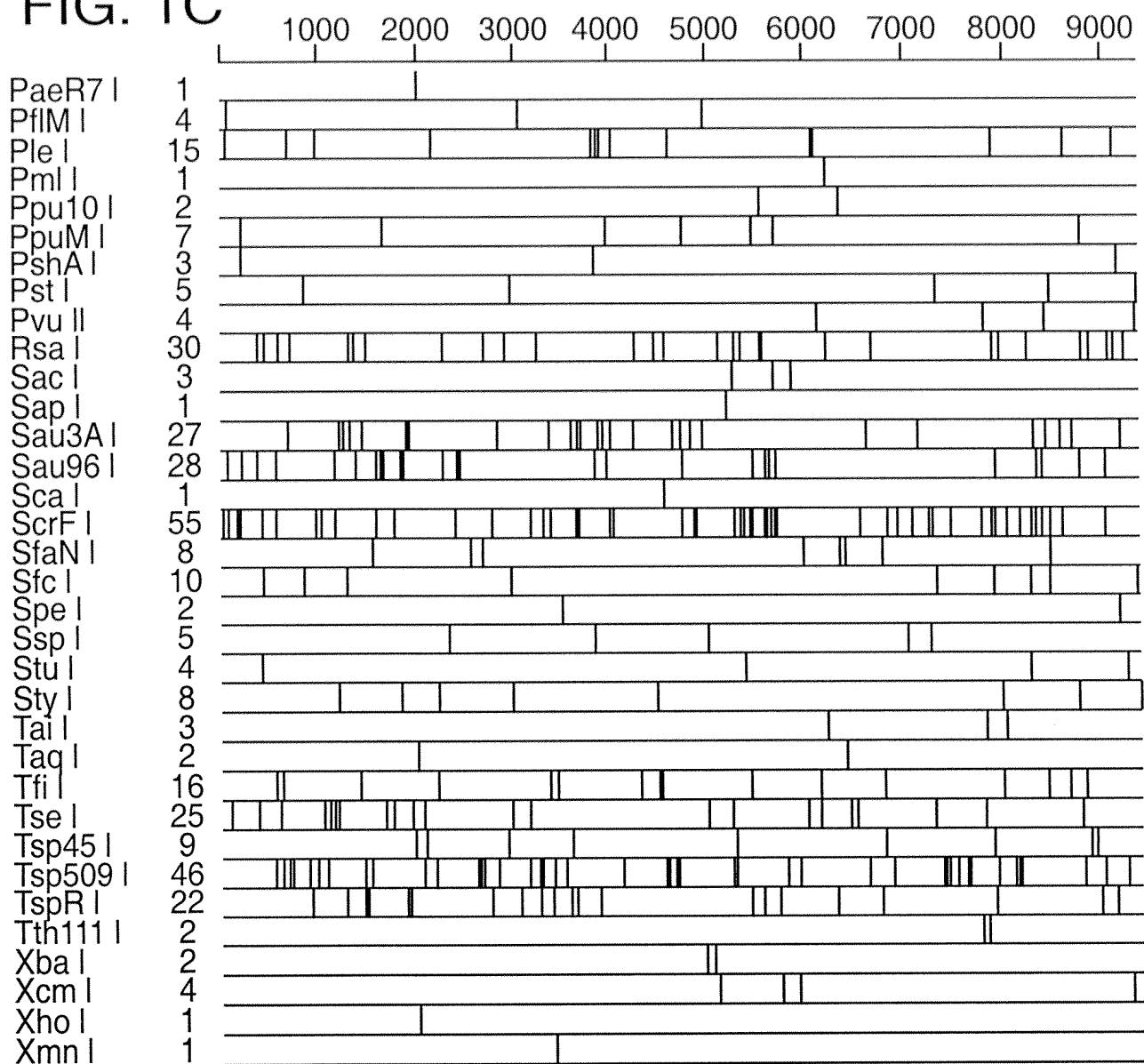


FIG. 1C



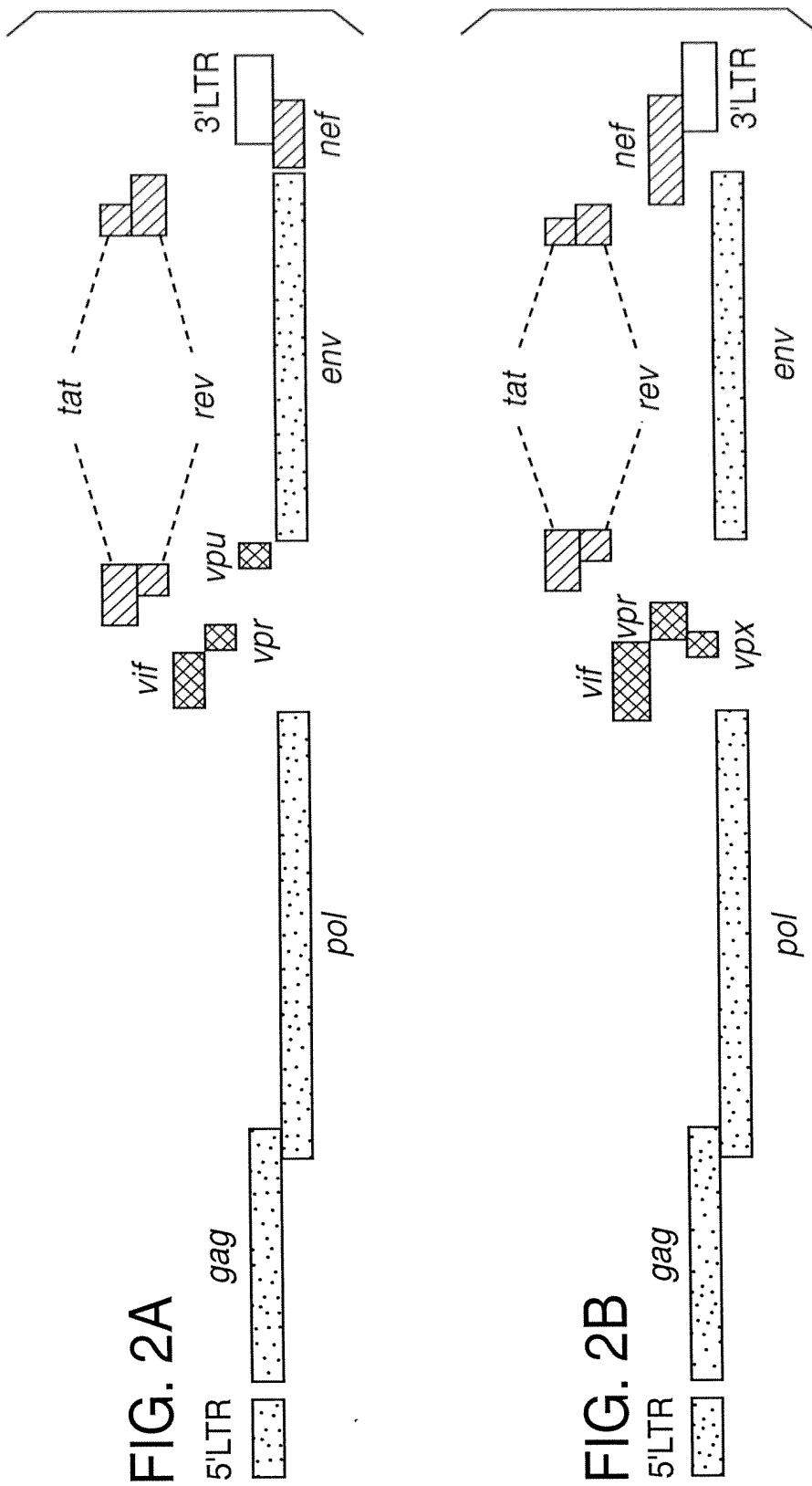


FIG. 3A
pROD(PK36) Leader Sequence

HIV2ROD ROD(PK36)	310	320	330	340	350
	GTTGGCGCCT	GAACAGGGAC	TTGAAGAAGA	CTGAGAACAGTC	TTGGAACACG
	GTTGGCGCCT	GAACAGGGAC	TTGAAGAAGA	CTGAGAACAGTC	TTGGAACACG
HIV2ROD ROD(PK36)	360	370	380	390	400
	GCTGAGTGAA	GGCAGTAAGG	GCAGGCAGGAA	CAAACCACGA	CGGAGTGCTC
	GCTGAGTGAA	GGCAGTAAGG	GCAGGCAGGAA	CAAACCACGA	CGGAGTGCTC
HIV2ROD ROD(PK36)	410	420	430	440	450
	CTAGAAAGGC	GCAGGCCGAG	GTACCAAAGG	CAGCGTGTGG	AGCGGGAGGA
	CTAGAAAGGC	GCAGGCCGAG	GTACCAAAGG	GAGCGTGTGG	AGCGGGAGGA
HIV2ROD ROD(PK36)	460	470	480	490	500
	GAAGAGGCCT	CCGGGTGAAG	GTAAGTACCT	ACACCAAAAA	CTGTAGCCGA
	GAAAGAGGCT	CCGGGTGAAG	GTAAGTACCT	ACACC	
HIV2ROD ROD(PK36)	510	520	530	540	550
	AAGGGCTTGC	TATCCTACCT	TTAGACAGGT	AGAAGATTGT	GGGAGATGGG
				T	GGGAGATGGG

FIG. 3B
pROD(SK36) Leader Sequence

HIV2ROD ROD(SK36)	310	320	330	340	350
	GTTGGCGCCT	GAACAGGGAC	TTGAAGAAGA	CTGAGAACAGTC	TTGGAACACG
	GTTGG				
HIV2ROD ROD(SK36)	360	370	380	390	400
	GCTGAGTGAA	GGCAGTAAGG	GCAGGCAGGAA	CAAACCACGA	CGGAGTGCTC
HIV2ROD ROD(SK36)	410	420	430	440	450
	CTAGAAAGGC	GCAGGCCGAG	GTACCAAAGG	CAGCGTGTGG	AGCGGGAGGA
HIV2ROD ROD(SK36)	460	470	480	490	500
	GAAGAGGCCT	CCGGGTGAAG	GTAAGTACCT	ACACCAAAAA	CTGTAGCCGA
	CT	CCGGGTGAAG	GTAAGTACCT	ACACCAAAAA	CTGTAGCCGA
HIV2ROD ROD(SK36)	510	520	530	540	550
	AAGGGCTTGC	TATCCTACCT	TTAGACAGGT	AGAAGATTGT	GGGAGATGGG
	AAGGGCTTGC	TATCCTACCT	TTAGACAGGT	AGAAGATTGT	GGGAGATGGG

FIG. 3C
pROD(SD36) Leader Sequence

HIV2ROD ROD(SD36)	310	320	330	340	350
	GTTGGCGCCT	GAACAGGGAC	TTGAAGAAGA	CTGAGAACAGTC	TTGGAACACCG
	GTTGG				
HIV2ROD ROD(SD36)	360	370	380	390	400
	GCTGAGTGAA	GGCAGTAAGG	GCGGCAGGAA	CAAACCACGA	CGGAGTGCTC
HIV2ROD ROD(SD36)	410	420	430	440	450
	CTAGAAAGGC	GCGGGCCGAG	GTACCAAAGG	CAGCGTGTGG	ACGGGGAGGA
HIV2ROD ROD(SD36)	460	470	480	490	500
	GAAGAGGCCT	CCGGGTGAAG	GTAAGTACCT	ACACCAAAAA	CTGTAGCCGA
	CT	CCGGGTGAAG	GTAAGTACCT	ACACC	
HIV2ROD ROD(SD36)	510	520	530	540	550
	AAGGGCTTGC	TATCCTACCT	TTAGACAGGT	AGAAGATTGT	GGGAGATGGG
				GT	GGGAGATGGG

FIG. 3D
pROD(CG36) Leader Sequence
(Designed and to be created)

HIV2ROD ROD(CG36)	310	320	330	340	350
	GTTGGCGCCT	GAACAGGGAC	TTGAAGAAGA	CTGAGAACAGTC	TTGGAACACCG
	GTTGGCGCCT	GAACAGGGAC	TTGAAGAAGA	CTGAGAACAGTC	TTGGAACACCG
HIV2ROD ROD(CG36)	360	370	380	390	400
	GCTGAGTGAA	GGCAGTAAGG	GCGGCAGGAA	CAAACCACGA	CGGAGTGCTC
	GCTGAGTGAA	GGCAGTAAGG			
HIV2ROD ROD(CG36)	410	420	430	440	450
	CTAGAAAGGC	GCGGGCCGAG	GTACCAAAGG	CAGCGTGTGG	ACGGGGAGGA
HIV2ROD ROD(CG36)	460	470	480	490	500
	GAAGAGGCCT	CCGGGTGAAG	GTAAGTACCT	ACACCAAAAA	CTGTAGCCGA
	CT	CCGGGTGAAG	GTAAGTACCT	ACACC	
HIV2ROD ROD(CG36)	510	520	530	540	550
	AAGGGCTTGC	TATCCTACCT	TTAGACAGGT	AGAAGATTGT	GGGAGATGGG
				GT	GGGAGATGGG

FIG. 3E

pROD(MR36) Leader Sequence (Designed and to be created)

HIV2ROD ROD(MR36)	310	320	330	340	350
	GTTGGCGCCT	GAACAGGGAC	TTGAAGAAGA	CTGAGAACGTC	TTGGAACACG
	GTTGG				
HIV2ROD ROD(MR36)	360	370	380	390	400
	GCTGAGTGAA	GGCAGTAAGG	GCGGCAGGAA	CAAACCACGA	CGGAGTGCTC
			GCGGCAGGAA	CAAACCACGA	CGGAGTGCTC
HIV2ROD ROD(MR36)	410	420	430	440	450
	CTAGAAAGGC	GCAGGGCCGAG	GTACCAAAGG	CAGCGTGTGG	AGCGGGAGGA
	CTAGAAAGGC	GCAGGGCCGAG	GTACCAAAGG	GAGCGTGTGG	AGCGGGAGGA
HIV2ROD ROD(MR36)	460	470	480	490	500
	GAAGAGGCCT	CCGGGTGAAG	GTAAGTACCT	ACACCAAAAA	CTGTAGCCGA
	GAAAGAGGCT	CCGGGTGAAG	GTAAGTACCT	ACACC	
HIV2ROD ROD(MR36)	510	520	530	540	550
	AAGGGCTTGC	TATCCTACCT	TTAGACAGGT	AGAAGATTGT	GGGAGATGGG
				GT	GGGAGATGGG

FIG. 4A

HIV-2 pROD(SD36/EM) Sequence of Mutant Region of Envelope
(Insertion mutant)

ROD	(6351)	ACAGAGGCTT TTGATGCAT	
EM		ACAGAGGCTT TTGATGCATA GGTAGCGTGA GATCTTAGTG CA	
ROD			G GAATAATA CA (6380)
EM		TAGGTAGC GTGAGATCTT AGTGCAAAGA TCGAATAATA CA	

FIG. 4B

pCM-ENV(ROD)(B-14)

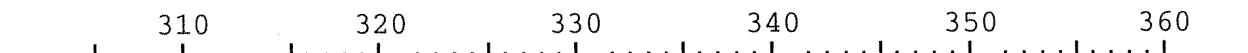
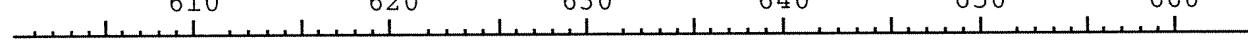
1	TCAATATTGG	CCATTAGCCA	TATTATTACAT	TGGTTATATA	GCATAAATCA
51	ATATTGGCTA	TTGGCCATTG	CATACGTTGT	ATCTATATCA	TAATATGTAC
101	ATTTATATTG	GCTCATGTCC	AATATGACCG	CCATGTTGGC	ATTGATTATT
151	GACTAGTTAT	TAATAGTAAT	CAATTACGGG	GTCATTAGTT	CATAGCCCAT
201	ATATGGAGTT	CCGCGTTACA	TAACTTACGG	TAAATGGCCC	GCCTGGCTGA
251	CCGCCAACG	ACCCCCGCC	ATTGACGTCA	ATAATGACGT	ATGTTCCCAT
301	AGTAACGCCA	ATAGGGACTT	TCCATTGACG	TCAATGGGTG	GAGTATTTAC
351	GGTAAACTGC	CCACTTGCGA	GTACATCAAG	TGTATCATAT	GCCAAGTCCG
401	CCCCCTATTG	ACGTCAATGA	CGGTAAATGG	CCCGCCTGGC	ATTATGCCA
451	GTACATGACC	TTACGGGACT	TTCCTACTTG	GCAGTACATC	TACGTATTAG
501	TCATCGCTAT	TACCATGGTG	ATGCCGTTTT	GGCAGTACAC	CAATGGCGT
551	GGATAGCGGT	TTGACTCACG	GGGATTTCCA	AGTCTCCACC	CCATTGACGT
601	CAATGGGAGT	TTGTTTGGC	ACCAAAATCA	ACGGGACTTT	CCAAAATGTC
651	GTAATAACCC	CGCCCCGTTG	ACGCAAATGG	GCGGTAGGCG	TGTACGGTGG
701	GAGGTCTATA	TAAGCAGAGC	TCGTTTAGTG	AACCGTCAGA	TCACTAGAAG
751	CTTTATTGCG	GTAGTTTATC	ACAGTTAAAT	TGCTAACGCA	GTCAGTGCTT
801	CTGACACAAAC	GGTCTCGAAC	TTAAGCTGCA	GAAGTTGGTC	GTGAGGCACT
851	GGGCAGGTAA	GTATCAAGGT	TACAAGACAG	GTTTAAGGAG	ACCAATAGAA
901	ACTGGGCTTG	TCGAGACAGA	GAAGACTCTT	GCGTTCTGA	TAGGCACCTA
951	TTGGTCTTAC	TGACATCCAC	TTTGCCTTTC	TCTCCACAGG	TGTCCACTCC
1001	CAGTTCAATT	ACAGCTCTTA	AGGCTAGAGT	ACTTAATACG	ACTCACTATA
1051	GGCTAGCCTC	GA		TACACCAGAC	AAGTGAGTAT 180
GATGAATCAG CTGCTTATTG CCATTTATT AGCTAGTGCT TGCTTAGTAT ATTGCACCCA 240					
ATATGTAACT GTTTCTATG GCGTACCCAC GTGGAAAAAT GCAACCATTG CCCTCTTTG 300					
					
310	320	330	340	350	360
TGCAACCAGA AATAGGGATA CTTGGGAAAC CATACTGTC TTGCCTGACA ATGATGATTA 360 TCAGGAAATA ACTTTGAATG TAACAGAGGC TTTTGATGCA TGGAAATAATA CAGTAACAGA 420 ACAAGCAATG AAAGATGTCT GGCATCTATT CGAGACATCA ATAAAACCAT GTGTCAAAC 480 AACACCTTTA TGTGTAGCAA TGAAATGCAG CAGCACAGAG AGCAGCATAG GGAACAAACAC 540 AACCTCAAAG AGCACAAGCA CAACCACAAC CACACCCACA GACCAGGAGC AAgagataag 600					
					
610	620	630	640	650	660
tgaggatact ccatgcgcac ggcgcagacaa ctgctcagga ttgggagagg aagaaacgt 660 caattgccag ttcaatatac caggattaga aagagataag aaaaaacagt ataatgaaac 720 atggtaactca aaagatgtgg tttgtgagac aaataatagc acaaatacaga cccagtgtt 780 catgaaccat tgcaacacat cagtcacatc agaatcatgt gacaaggact attggatgc 840 tataaggttt agatactgtg caccaccggg ttatgcccta ttaagatgta atgataccaa 900					

FIG. 4C

910 920 930 940 950 960
ttattcaggc tttgcaccca actgttctaa agtagtagct tctacatgca ccaggatgat 960
ggaaaccaa acttccacat ggttggctt taatggact agagcagaga atagaacata 1020
tatctattgg catggcagag ataatagaac tatcatcagc ttaaacaaaat attataatct 1080
cagttgcat tgtaagaggc cagggataa gatagtgaaa caaataatgc ttatgtcagg 1140
acatgtgtt cactcccact accagccat caataaaaga cccagacaag catggtgctg 1200
1210 1220 1230 1240 1250 1260
gttcaaaggc aaatggaaaag acgccatgca ggaggtgaag gaaacccttg caaaacatcc 1260
caggtataga ggaaccaatg acacaaggaa tattagctt gcagcgccag gaaaaggctc 1320
agacccagaa gtagcataca tgtggactaa ctgcagagga gagtttctct actgcaacat 1380
gacttggttc ctcaattgga tagagaataa gacacaccgc aattatgcac cgtgccatat 1440
aaagcaaata attaacacat ggcataaggt agggagaaat gtatattgc ctcccaggg 1500
1510 1520 1530 1540 1550 1560
aggggagctg tcctgcaact caacagtaac cagcataatt gctaacattt actggcaaaa 1560
caataatcg acaaacatta ccttagtgc agaggtggca gaactataca gattggagtt 1620
gggagattat aaattggtag aaataaacacc aattggcttc gcacctacaa aaaaaaaaag 1680
atactcctct gtcacggga gacatacaag aggtgtttc gtgctagggt tcttgggtt 1740
tctcgcaaca gcaggttctg caatggcgc ggcgtccctg accgtgtcgg ctcagtcccc 1800
1810 1820 1830 1840 1850 1860
gactttactg gccgggatacg tgcagcaaca gcaacagctg ttggacgtgg tcaagagaca 1860
acaagaactg ttgcgactga ccgtctgggg aacaaaaac ctccaggcaa gagtcactgc 1920
tatagagaag tacctacagg accaggcgcg gctaaattca tggggatgtg cgtttagaca 1980
agtctgccac actactgtac catgggttaa tgattcctta gcacctgact gggacaatat 2040
gacgtggcag gaatggaaaa aacaagtccg ctacctggag gcaaataatca gtaaaagttt 2100
2110 2120 2130 2140 2150 2160
agaacaggca caaattcagc aagagaaaaa tatgtatgaa ctacaaaaat taaaatagctg 2160
ggatatttt ggcaatttgtt ttgacttaac ctcctgggtc aagtatattc aatatggagt 2220
gcttataata gtagcagtaa tagcttaag aatagtgata tatgttagtac aaatgttaag 2280
taggcttaga aagggtataa ggcctgtttt ctcttcccc cccggttata tccaacagat 2340
ccatatccac aaggaccggg gacagccagc caacgaagaa acagaagaag acggtgaaag 2400
2410 2420 2430 2440 2450 2460
caacggtgga gacagatact ggccctggcc gatagcaTAT ATACATTTCC TGATCCGCCA 2460
GCTGATTGCG CTCTTGACCA GACTATACAG CATCTGCAGG GACTTACTAT CCAGGAGCTT 2520
CCTGACCCTC CAACTCATCT ACCAGAACATCT CAGAGACTGG CTGAGACTTA GAACAGCCTT 2580
CTTGCAATAT GGGTGCAGT GGATCCAAGA AGCATTCAG GCCGCCGCGA GGGCTACAAG 2640
AGAGACTCTT GCGGGCGCGT GCAGGGGCTT GTGGAGGGTA TTGGAACGAA TCGGGAGGGG 2700
2710 2720 2730 2740 2750 2760
AATACTCGCG GTTCCAAGAAA GGATCAGACA GGGAGCAGAA ATCGCCTCCT GTGAGGGACG 2760
GCAGTATAGC CAGGGAGACT TTATGAATAC TCCATGG

FIG. 4D

					GGCGG
1101	CCGCTTCGAG	CAGACATGAT	AAGATACATT	GATGAGTTG	GACAAACCAC
1151	AACTAGAATG	CAGTGAAAAA	AATGCTTAT	TTGTGAAATT	TGTGATGCTA
1201	TTGCTTTATT	TGTAACCATT	ATAAGCTGCA	ATAAACAAAGT	TAACAACAAAC
1251	AATTGCATTC	ATTTTATGTT	TCAGGTTCA	GGGGAGATGT	GGGAGGTTTT
1301	TTAAAGCAAG	TAAAACCTCT	ACAAATGTGG	TAAAATCGAT	AAGGATCCGG
1351	GCTGGCGTAA	TAGCGAAGAG	GCCCCCACCG	ATCGCCCTTC	CCAACAGTTG
1401	CGCAGCCTGA	ATGGCGAATG	GACGCGCCCT	GTAGCGGC	ATTAAGCGCG
1451	GCGGGTGTGG	TGGTTACGCG	CAGCGTGACC	GCTACACTTG	CCAGCGCCCT
1501	AGCGCCCGCT	CCTTTCGCTT	TCTTCCCTTC	CTTTCTCGCC	ACGTTCGCCG
1551	GCTTTCCCCG	TCAAGCTCTA	AATCGGGGGC	TCCCTTTAGG	GTTCCGATT

FIG. 4E

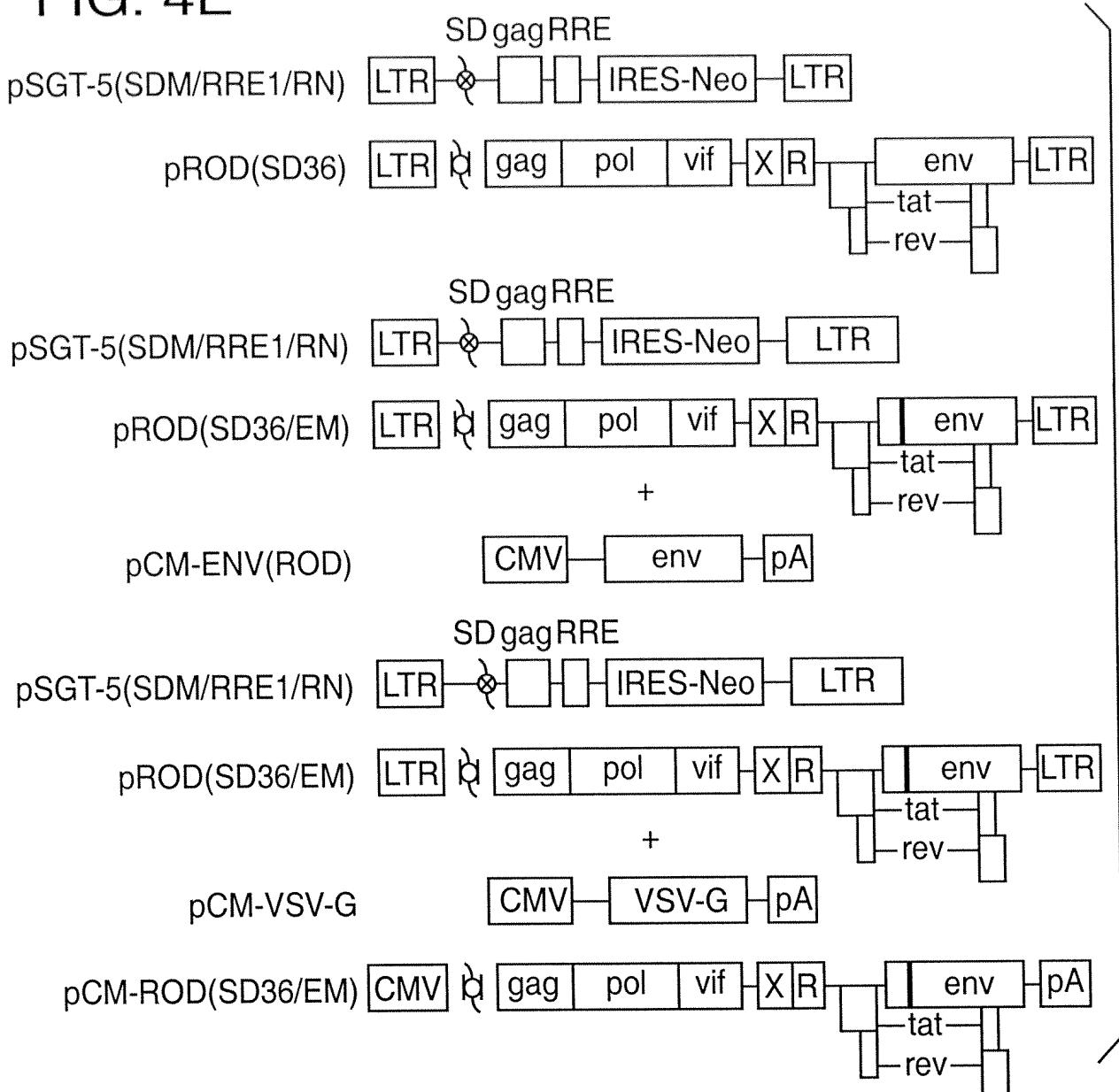


FIG. 5A

SIV 5' LTR Leader Sequence

R→	10	20	30	40	50
	GCTCTGTATT	CAGTCGCTCT	GCGGAGAGGC	TGGCAGATTG	AGCCCTGGGA
	60	70	80	90	100
	GGTTCTCTCC	AGCACTAGCA	GGTAGAGCCT	GGGTGTTCCC	TGCTAGACTC
	110	120	130	140	150
	TCACCAGCAC	TTGGCCGGTG	CTGGGCAGAG	TGACTCCACG	CTTGCTTGCT
	160	170	180	190	200
	TAAAGCCCTC	TTCAATAAAG	CTGCCATTTT	AGAACGTAAGC	TAGTGTGTGT
	210	220	230	240	250
	TCCCCATCTCT	CCTAGCCGCC	GCCTGGTCAA	CTCGGTACTC	AATAATAAGA
	260	270	280	290	300
	AGACCCCTGGT	CTGTTAGGAC	CCTTTCTGCT	TTGGGAAACC	GAAGCAGGAA
	310	320	330	340	350
	AATCCCTAGC	AGATTGGCGC	CTGAACAGGG	ACTTGAAGGA	GAGTGAGAGA
	360	370	380	390	400
	CTCCTGAGTA	CGGCTGAGTG	AAGGCAGTAA	GGGCGGCAGG	AACCAACCAC
	410	420	430	440	450
	GACGGAGTC	TCCTATAAAG	GCGCGGGTCG	GTACCAGACG	GCGTGAGGAG
	460	470	480	490	500
	CGGGAGAGGA	AGAGGCCTCC	GGTTGCAGGT	AAGTGCAACA	CAAAAAAGAA
	510	520	530	540	550
	ATAGCTGTCT	TTTATCCAGG	AAGGGGTAAT	AAGATAGAGT	GGGAGATGGG
	560				
	CGTGAGAAC				

FIG. 5B

pSIV(SD36)

	320	330	340	350	360
WTL SD36	GATTGGCGC GATTGG	CTGAACAGGG	ACTTGAAGGA	GAGTGAGAGA	CTCCTGAGTA
	370	380	390	400	410
WTL SD36	CGGCTGAGTG	AAGGCAGTAA	GGGCGGCAGG	AACCAACCAC	GACGGAGTGC
	420	430	440	450	460
WTL SD36	TCCTATAAAAG	GCGCGGGTCG	GTACCAGACG	GCGTGAGGAG	CGGGAGAGGA
	470	SD 480	490	500	510
WTL SD36	AGAGGCCTCC CTCC	GGTTGCAGGT GGTTGCAGGT	AAGTGCAACA AAGTGCAACA	CAAAAAAGAA CA	ATAGCTGTCT
	520	530	540	550	560
WTL SD36	TTTATCCAGG	AAGGGGTAAT	AAGATAGAGT GT	GGGAGATGGG GGGAGATGGG	CGTGAGAAC CGTGAGAAC

FIG. 5C

pSIV(SDM)

	320	330	340	350	360
WTL	GATTGGCGC	CTGAACAGGG	ACTTGAAGGA	GAGTGAGAGA	CTCCTGAGTA
SDM	GATTGGCGC	CTGAACAGGG	ACTTGAAGGA	GAGTGAGAGA	CTCCTGAGTA
	370	380	390	400	410
WTL	CGGCTGAGTG	AAGGCAGTAA	GGGCAGGCAGG	AACCAACCAC	GACGGAGTGC
SDM	CGGCTGAGTG	AAGGCAGTAA	GGGCAGGCAGG	AACCAACCAC	GACGGAGTGC
	420	430	440	450	460
WTL	TCCTATAAAAG	GCGCGGGTCG	GTACCAGACG	GCGTGAGGAG	CGGGAGAGGA
SDM	TCCTATAAAAG	GCGCGGGTCG	GTACCAGACG	GCGTGAGGAG	CGGGAGAGGA
	SD				
	470	480	490	500	510
WTL	AGAGGCCTCC	GGTTGCAGGT	AAGTGCAACA	AAAAAAAGAA	ATAGCTGTCT
SDM	AGAGGCCTCC	GGTTGATATC	GAGTGCAACA	AAAAAAAGAA	ATAGCTGTCT
	520	530	540	550	560
WTL	TTTATCCAGG	AAGGGGTAAT	AAGATAGAGT	GGGAGATGGG	CGTGAGAAC
SDM	TTTATCCAGG	AAGGGGTAAT	AAGATAGAGT	GGGAGATGGG	CGTGAGAAC

FIG. 6A

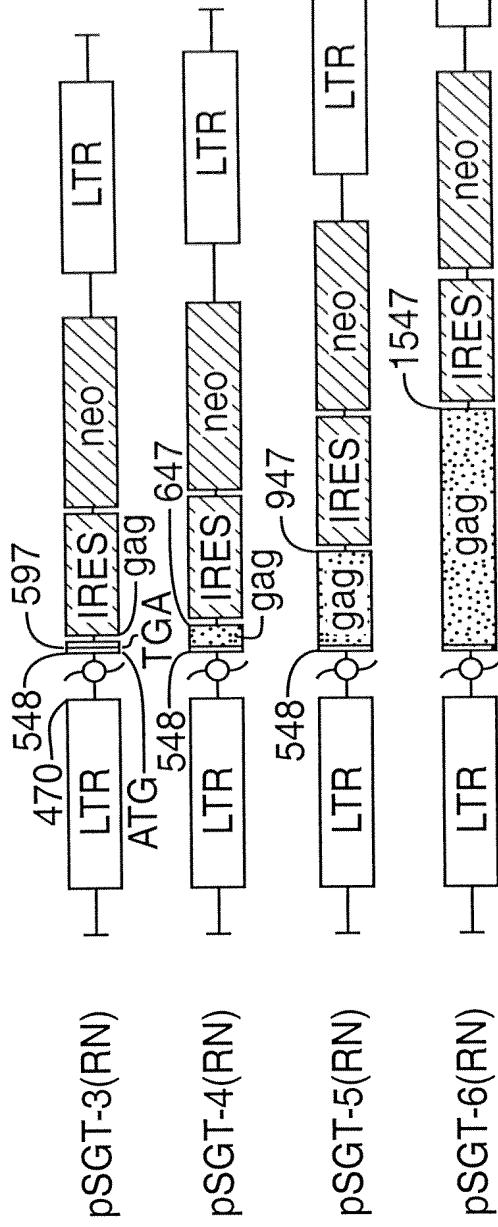


FIG. 6B

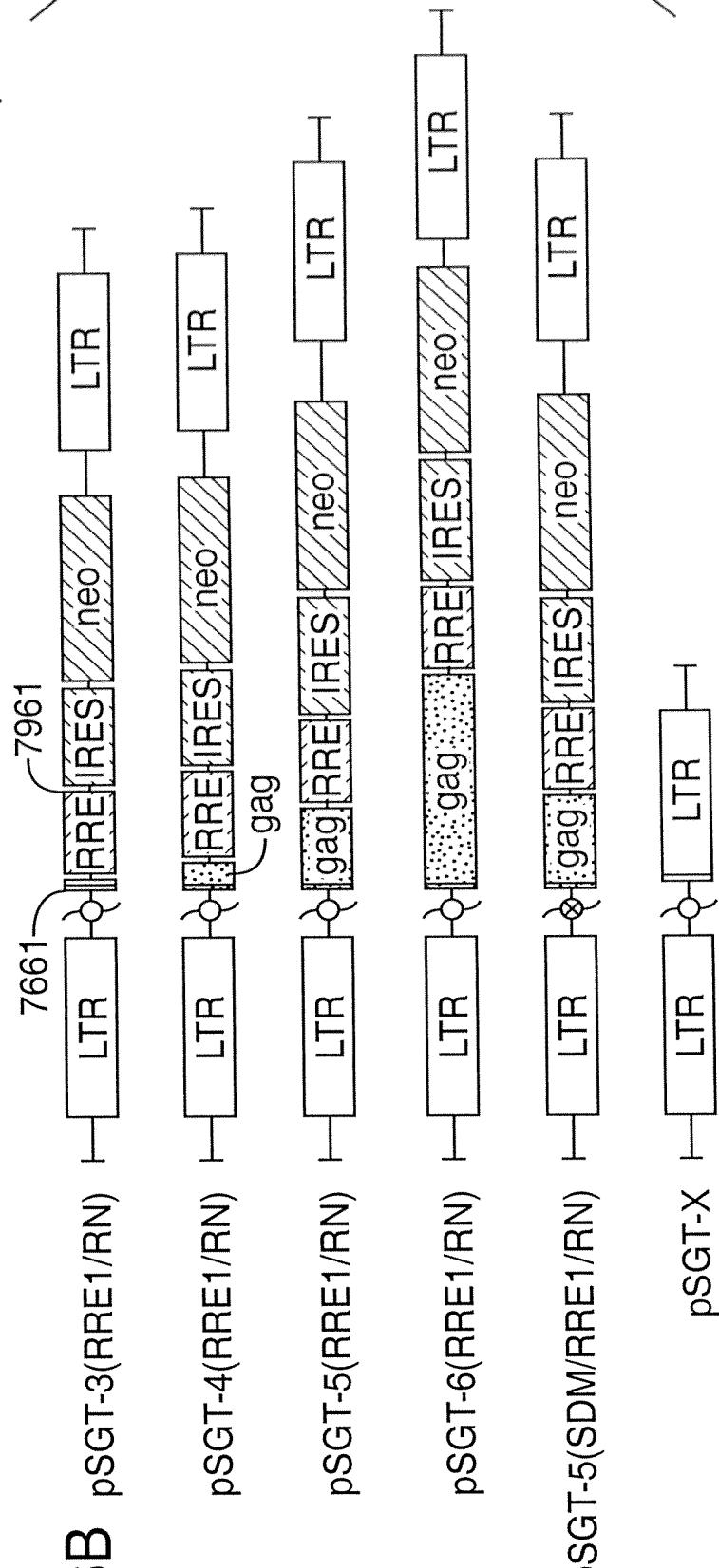


FIG. 7A

pSGT5(SDM/RR)

|U3 -530 -520
GGAA GGGCTGTATT ACAGTGATAG

-530 -520 -510 -500 -490 -480
GAGACGTAGA GTCCTAGACA TATACTTAGA AAAGGAAGAG GGAATAATTG GAGACTGGCA

-470 -460 -450 -440 -430 -420
GAACCTACT CATG GACCAG GAGTAAGGTA TCCAAAGTTTC TTTGGGTGGT TATGGAAGCT

-410 -400 -390 -380 -370 -360
AGTACCACTA GATGTCCCAC AAAGA GGGAGA TGACAGTGAG ACTCACTGCT TAGTGCATCC

-350 -340 -330 -320 -310 -300
AGCA CAAACA AGCAGGTTTG ATGACCCGCA TGGAGAAACA TTAGTTGGA GGTTGACCC

-290 -280 -270 -260 -250 -240
CACGCTAGCT TTTAGCTACG AGGCCTTAT TCGATACCCA GAGGAGTTTG GGTACAAGTC

-230 -220 -210 -200 -190 -180
AGGCCTGCCA GAGGATGAAT GGAAGGCAAG ACTGAAAGCA AGAGGGATAC CGTTAGCTA

-170 -160 -150 -140 -130 -120
AAAACAGGAA CAGCTATACT TGGTCAGGGC AGGAAGTAAC TAACAGAAAA CAGCTGAGAC

-110 -100 -90 -80 -70 -60
TGCAGGGACT TTCCAGAAGG GGCTGTTACC AGGGGAGGGGA CATGGGAGGA GCCGGTGGGG

-50 -40 -30 -20 -10 U3|
AACGCCCTCA TACTTCTGT ATAAATGTAC CCGCTACTCG CATTGTATTC

|R 10 20 30 40 50 60
GTTCGCTCTG CGGAGAGGCT GGCAGATTGA GCCCTGGAG GTTCTCTCCA GCACTAGCAG

70 80 90 100 110 120
TGGTCACCTG GGTGTTCCCT GCTAGACTCT CACCAGTGCT TGGCCGGCAC TGGCAGACG

130 140 150 160 170 R|U5 180
GCTCCACGCT TGCTTGCTTA AAAGACCTCT TAATAAAGCT GCCAGTTAGA AGCAAGTTAA

190 200 210 220 230 240
GTGTGTGCTC CCATCTCTCC TAGTCGCCGC CTGGTCATTG GGTGTTCATC TAAAGTAACA

250 260 270 280 290 300
AGACCCCTGGT CTGTTAGGAC CCTTTCTGCT TTGGGAAACC AAGGCAGGAA AATCCCTAGC

U5|Leader 310 320 330 340 350 360
AGGTTGGCGC CCGAACAGGG ACTTGAAGAA GACTGAGAAG CCTTGAACA CGGCTGAGTG

370 380 390 400 410 420
AAGGCAGTAA GGGCGGCAGG AACAAACCAC GACGGAGTGC TCCTAGAAAA GCGCAGGCCG

FIG. 7B

430 440 450 460 470|---SDM---| 480
AGGTACCAAG GGCAGCGTGT GGAGCGGGAG TGAAAGAGGC CTCCGGGTGA TATCAGTGCC

490 500 510 520 530 540
TACACCAAAT ACAGTAGCCA GAAGGGCTTG TTATCCTACC TTTAGACGGG TAGAAGATTG

Leader |gag 560 570 580 590 600
TGGGAGATGC CATGGTAGGG CGCGAGAAC TCCGTCTTGA GAGGGAAAAA AGCAGACGAA

610 620 630 640 650 660
TTAGAAAAGA TTAGGTTACG GCCCGGCCGA AAGAAAAAAT ATAGGCTAAA ACATATTGTG

670 680 690 700 710 720
TGGGCAGCGA ATGAATTGGA CAGATTCGGA TTGGCAGAGA GCCTGTTGGA GTCAAAAGAG

730 740 750 760 770 780
GGTTGCCAAAA AAATTCTTAC AGTTTAGAT CCATTAGTAC CGACAGGGTC AGAAAATTAA

790 800 810 820 830 840
AAAAGCCTTT TTAATACTGT CTGCGTCATT TGGTGTATAC ACGCAGAAGA GAAAGCGAAA

850 860 870 880 890 900
GATACTGAAG AAGCAAAACA AAAGGTACAG AGACATCTAG TGGCAGAAAC AAAAAACTACA

910 920 930 940 950gag(955) |poly(L)
GAAAAAAATGC CAAGTACAAG TAGACCAACA GCACCACCTA GCGGGAACCG AGGAACCTCGA

970 980 | RRE(7661) 990 1000 1010 1020
ATGCATGGTG ACCGCGGCCG CAGAGGTGTA TTCGTGCTAG GGTTCTTAGG TTTCTCACA

1030 1040 1050 1060 1070 1080
GCAGGAGCTG CAATGGGCAC GGCCTCCTTG ACGCTGTCGG CTCAGTCTCG GACTTTATTG

1090 1100 1110 1120 1130 1140
GCCGGGATAG TGCAGCAACA GCAACAGCTG TTGGACGTGG TCAAGAGACA ACAAGAAATG

1150 1160 1170 1180 1190 1200
TTGCGACTGA CCGTCTGGGG AACAAAAAAT CTCCAGGCAA GAGTCACTGC TATCGAGAAA

1210 1220 1230 1240 1250 1260
TACTTAAAGG ACCAGGCGC AACTAAATTCA TGGGGATGTG CGTCTAGACA AGTCTGCCAC

1270 RRE(7960)| poly(L) 1290 |(8770) 1310 1320
ACTACTGTAC CATGGGTAGC GGCGCTCGC GAGTAGACCA TGGAGAGCCC CAGCAGAAAGG

1330 1340 1350 1360 1370 1380
GGAGAAAGGC TCGTACAAGC AACAAAATAT GGATGATGTA GATTCAAGATG ATGATGACCT

1390 1400 1410 1420 1430 1440
AGTAGGGGTC CCTGTCACAC CAAGAGTACC ATTAAGAGAA ATGACATATA GGTTGGCAAG

1450 1460 1470 (8944)U3 1480 1490 1500
AGAT ATGTCA CATTGATAA AAGAAAAGGG GGGACTGGAA GGGCTGTATT ACAGTGATAG

FIG. 7C

1510 1520 1530 1540 1550 1560
GAGACGTAGA GTCCTAGACA TATACTTAGA AAAGGAAGAG GGAATAATTG GAGACTGGCA

1570 1580 1590 1600 1610 1620
GAACCTACT CATG GACCA GAGTAAGGTA TCCAAAGTTC TTTGGGTGGT TATGGAAGCT

1630 1640 1650 1660 1670 1680
AGTACCACTA GATGTCCCAC AAGA GGGAGA TGACAGTGAG ACTCACTGCT TAGTGCATCC

1690 1700 1710 1720 1730 1740
AGCA CAAACA AGCAGGTTG ATGACCCGCA TGGAGAAACA TTAGTTTGGA GGTTGACCC

1750 1760 1770 1780 1790 1800
CACGCTAGCT TTTAGCTACG AGGCCTTAT TCGATACCCA GAGGAGTTG GGTACAAGTC

1810 1820 1830 1840 1850 1860
AGGCCTGCCA GAGGATGAAT GGAAGGCAAG ACTGAAAGCA AGAGGGATAC CGTTAGCTA

1870 1880 1890 1900 1910 1920
AAAACAGGAA CAGCTACTA TGGTCAGGGC AGGAAGTAAC TAACAGAAAA CAGCTGAGAC

1930 1940 1950 1960 1970 1980
TGCAGGGACT TTCCAGAAGG GGCTGTTACC AGGGGAGGGA CATGGGAGGA GCCGGTGGGG

1990 2000 2010 2020 U3|R 2040
AACGCCCTCA TACTTCTGT ATAAATGTAC CCGCTACTCG CATTGTATTG AGTCGCTCTG

2050 2060 2070 2080 2090 2100
CGGAGAGGCT GGCAGATTGA GCCC TGGGAG GTTCTCTCCA GCACTAGCAG GTAGGCCTG

2110 2120 2130 2140 2150 2160
GGTGTCCCT GCTAGACTCT CACCAAGTGC TGGCCGGCAC TGGGCAGACG GCTCCACGCT

2170 2180 2190 R|
TGCTTGCTTA AAAGACCTCT TAATAAAGC TGCCA

FIG. 7D

10	20	30	40	50	60
TCTAGAGGAA	TTCCGGCCCT	CTCCCTCCCC	CCCCCCTAAC	GTTACTGGCC	GAAGCCGCTT
70	80	90	100	110	120
GGAATAAGGC	CGGTGTGCGT	TTGTCTATAT	GTTATTTTCC	ACCATATTGC	CGTCTTTG
130	140	150	160	170	180
CAATGTGAGG	GCCCGGAAAC	CTGGCCCTGT	CTTCTTGACG	AGCATTCCCA	GGGGTCTTTC
190	200	210	220	230	240
CCCTCTCGCC	AAAGGAATGC	AAGGTCTGTT	GAATGTCGTG	AAGGAAGCAG	TTCCCTCTGGA
250	260	270	280	290	300
AGCTTCTTGA	AGACAAAACAA	CGTCTGTAGC	GACCCTTTGC	AGGCAGCGGA	ACCCCCCAC
310	320	330	340	350	360
TGGCGACAGG	TGCCTCTGCG	GCCAAAAGCC	ACGTGTATAA	GATACACCTG	CAAAGGCGGC
370	380	390	400	410	420
ACAACCCCAG	TGCCACGTTG	TGAGTTGGAT	AGTTGTGGAA	AGAGTCAAAT	GGCTCTCCTC
430	440	450	460	470	480
AAGCGTATTG	AACAAGGGGC	TGAAGGATGC	CCAGAAGGTA	CCCCATTGTA	TGGGATCTGA
490	500	510	520	530	540
TCTGGGGCCT	CGGTGCACAT	GCTTTACATG	TGTTTAGTCG	AGGTTAAAAA	ACGTCTAGGC
550	560	570	580	590	600
CCCCCGAACCC	ACGGGGACGT	GGTTTCCTT	TGAAAAAACAC	GATGATAAGC	TTGCCACAAAC
610	620	630	640	650	660
CATGGCTGAA	CAAGATGGAT	TGCACGCAGG	TTCTCCGGCC	GCTTGGGTGG	AGAGGCTATT
670	680	690	700	710	720
CGGCTATGAC	TGGGCACAAC	AGACAATCGG	CTGCTCTGAT	GCCGCCGTGT	TCCGGCTGTC
730	740	750	760	770	780
AGCGCAGGGG	CGCCCGGTT	TTTTTGTCAA	GACCGACCTG	TCCGGTGCCC	TGAATGAACT
790	800	810	820	830	840
GCAGGACGAG	GCAGCGGGC	TATCGTGGCT	GGCCACGACG	GGCGTTCCCT	GCGCAGCTGT
850	860	870	880	890	900
GCTCGACGTT	GTCACTGAAG	CGGGAAGGGA	CTGGCTGCTA	TTGGGCGAAG	TGCCGGGGCA
910	920	930	940	950	960
GGATCTCCTG	TCATCTCAC	TTGCTCCTGC	CGAGAAAGTA	TCCATCATGG	CTGATGCAAT
970	980	990	1000	1010	1020
GCGGCGGCTG	CATACGCTTG	ATCCGGCTAC	CTGCCCATTG	GACCACCAAG	CGAAACATCG
1030	1040	1050	1060	1070	1080
CATCGAGCGA	GCACGTACTC	GGATGGAAGC	CGGTCTTGTC	GATCAGGATG	ATCTGGACGA
1090	1100	1110	1120	1130	1140
AGAGCATCAG	GGGCTCGCGC	CAGCCGAAC	GTTCGCCAGG	CTCAAGGCGC	GCATGCCCGA
1150	1160	1170	1180	1190	1200
CGGCGAGGAT	CTCGTCGTGA	CCCATGGCGA	TGCCTGTTG	CCGAATATCA	TGGTGGAAAA
1210	1220	1230	1240	1250	1260
TGGCCGCTT	TCTGGATTCA	TCGACTGTGG	CCGGCTGGGT	GTGGCGGACC	GCTATCAGGA
1270	1280	1290	1300	1310	1320
CATAGCGTTG	GCTACCCGTG	ATATTGCTGA	AGAGCTTGGC	GGCGAATGGG	CTGACCGCTT
1330	1340	1350	1360	1370	1380
CCTCGTGCTT	TACGGTATCG	CCGCTCCCGA	TTCGCAGCGC	ATCGCCTTCT	ATCGCCTTCT
1390	1400	1410	C		
TGACGAGTTC	TTCTGAGCGG	GATCGGCTAG			

FIG. 7E

pSGT-5(SDM) 5'LTR-Leader Sequence

	10	20	30	40	50
HIV2ST	GTTCGCTCTG	CGGAGAGGCT	GGCAGATTGA	GCCCTGGGAG	GTTCTCTCCA
pSGT5(SDM)	GTTCGCTCTG	CGGAGAGGCT	GGCAGATTGA	GCCCTGGGAG	GTTCTCTCCA
	60	70	80	90	100
HIV2ST	GCACTAGCAG	TGGTCACCTG	GGTGTCCCT	GCTAGACTCT	CACCAAGTGCT
pSGT5(SDM)	GCACTAGCAG	TGGTCACCTG	GGTGTCCCT	GCTAGACTCT	CACCAAGTGCT
	110	120	130	140	150
HIV2ST	TGGCCGGCAC	TGGGCAGACG	GCTCCACGCT	TGCTTGCTTA	AAAGACCTCT
pSGT5(SDM)	TGGGCAGCAC	TGGGCAGACG	GCTCCACGCT	TGCTTGCTTA	AAAGACCTCT
	160	170	180	190	200
HIV2ST	TAATAAAGCT	GCCAGTTAGA	AGCAAGTTAA	GTGTGTGCTC	CCATCTCTCC
pSGT5(SDM)	TAATAAAGCT	GCCAGTTAGA	AGCAAGTTAA	GTGTGTGCTC	CCATCTCTCC
	210	220	230	240	250
HIV2ST	TAGTCGCCGC	CTGGTCATTG	GGTGTTCATC	TAAAGTAACA	AGACCCTGGT
pSGT5(SDM)	TAGTCGCCGC	CTGGTCATTG	GGTGTTCATC	TAAAGTAACA	AGACCCTGGT
	260	270	280	290	300
HIV2ST	CTGTTAGGAC	CCTTCTGCT	TTGGGAAACC	AAGGCAGGAA	AATCCCTAGC
pSGT5(SDM)	CTGTTAGGAC	CCTTCTGCT	TTGGGAAACC	AAGGCAGGAA	AATCCCTAGC
	310	320	330	340	350
HIV2ST	AGGTTGGCGC	CCGAACAGGG	ACTTGAAGAA	GAUTGAGAAG	CCTTGGAAACA
pSGT5(SDM)	AGGTTGGCGC	CCGAACAGGG	ACTTGAAGAA	GAUTGAGAAG	CCTTGGAAACA
	360	370	380	390	400
HIV2ST	CGGCTGAGTG	AAGGCAGTAA	GGGCGGCAGG	AACAAACCAC	GACGGAGTGC
pSGT5(SDM)	CGGCTGAGTG	AAGGCAGTAA	GGGCGGCAGG	AACAAACCAC	GACGGAGTGC
	410	420	430	440	450
HIV2ST	TCCTAGAAAA	GCGCAGGCCG	AGGTACCAAG	GGCGGCGTGT	GGAGCGGGAG
pSGT5(SDM)	TCCTAGAAAA	GCGCAGGCCG	AGGTACCAAG	GGCGGCGTGT	GGAGCGGGAG
	460	470	480	490	500
HIV2ST	TGAAAGAGGC	CTCCGGGTGA	AGGTAAGTGC	CTACACCAAA	TACAGTAGCC
pSGT5(SDM)	TGAAAGAGGC	CTCCGGGTGA	TATC AGTGC	CTACACCAAA	TACAGTAGCC
	510	520	530	540	550
HIV2ST	AGAAGGGCTT	GTTATCCTAC	CTTAGACGG	GTAGAAGATT	GTGGGAGATG
pSGT5(SDM)	AGAAGGGCTT	GTTATCCTAC	CTTAGACGG	GTAGAAGATT	GTGG AGATG

FIG. 7F

pSGT-5(SDM) Leader Sequence

HIV2ST	310	320	330	340	350
pSGT5(SDM)	AGGTTGGCGC	CCGAACAGGG	ACTTGAAGAA	GACTGAGAAG	CCTTGGAAC
	AGGTTGGCGC	CCGAACAGGG	ACTTGAAGAA	GACTGAGAAG	CCTTGGAAC
HIV2ST	360	370	380	390	400
pSGT5(SDM)	CGGCTGAGTG	AAGGCAGTAA	GGGCGGCAGG	AACAAACCAC	GACGGAGTGC
	CGGCTGAGTG	AAGGCAGTAA	GGGCGGCAGG	AACAAACCAC	GACGGAGTGC
HIV2ST	410	420	430	440	450
pSGT5(SDM)	TCCTAGAAAA	GCGCAGGCCG	AGGTACCAAG	GGCGGCGTGT	GGAGCGGGAG
	TCCTAGAAAA	GCGCAGGCCG	AGGTACCAAG	GGCGGCGTGT	GGAGCGGGAG
	SD				
HIV2ST	460	470	480	490	500
pSGT5(SDM)	TGAAAGAGGC	CTCCGGGTGA	AGGTAAAGTGC	CTACACCAAA	TACAGTAGCC
	TGAAAGAGGC	CTCCGGGTGA	TATC AGTGC	CTACACCAAA	TACAGTAGCC
HIV2ST	510	520	530	540	550
pSGT5(SDM)	AGAAGGGCTT	GTTATCCTAC	CTTAGACGG	GTAGAAGATT	GTGGGAGATG
	AGAAGGGCTT	GTTATCCTAC	CTTAGACGG	GTAGAAGATT	GTGG AGATG

FIG. 7G

pSGT-5(SDX) Leader Sequence

HIV2ST	310	320	330	340	350
pSGT5(SDX)	AGGTTGGCGC	CCGAACAGGG	ACTTGAAGAA	GACTGAGAAG	CCTTGGAACCA
	AGGTTGGCGC	CCGAACAGGG	ACTTGAAGAA	GACTGAGAAG	CCTTGGAACCA
HIV2ST	360	370	380	390	400
pSGT5(SDX)	CGGCTGAGTG	AAGGCAGTAA	GGGCAGGCAGG	AACAAACCAC	GACGGAGTGC
	CGGCTGAGTG	AAGGCAGTAA	GGGCAGGCAGG	AACAAACCAC	GACGGAGTGC
HIV2ST	410	420	430	440	450
pSGT5(SDX)	TCCTAGAAAA	GCGCAGGCCG	AGGTACCAAG	GGCGGCGTGT	GGAGCGGGAG
	TCCTAGAAAA	GCGCAGGCCG	AGGTACCAAG	GGCGGCGTGT	GGAGCGGGAG
HIV2ST	460	470	480	490	500
pSGT5(SDX)	TGAAAGAGGC	CTCCGGGTGA	AGGTAAGTGC	CTACACCAAA	TACAGTAGGCC
	TGAAAGAGGC	CTCCGG	GC	CTACACCAAA	TACAGTAGGCC
HIV2ST	510	520	530	540	550
pSGT5(SDX)	AGAAGGGCTT	GTTATCCTAC	CTTAGACGG	GTAGAAGATT	GTGGGAGATG
	AGAAGGGCTT	GTTATCCTAC	CTTAGACGG	GTAGAAGATT	GTGG AGATG

FIG. 8

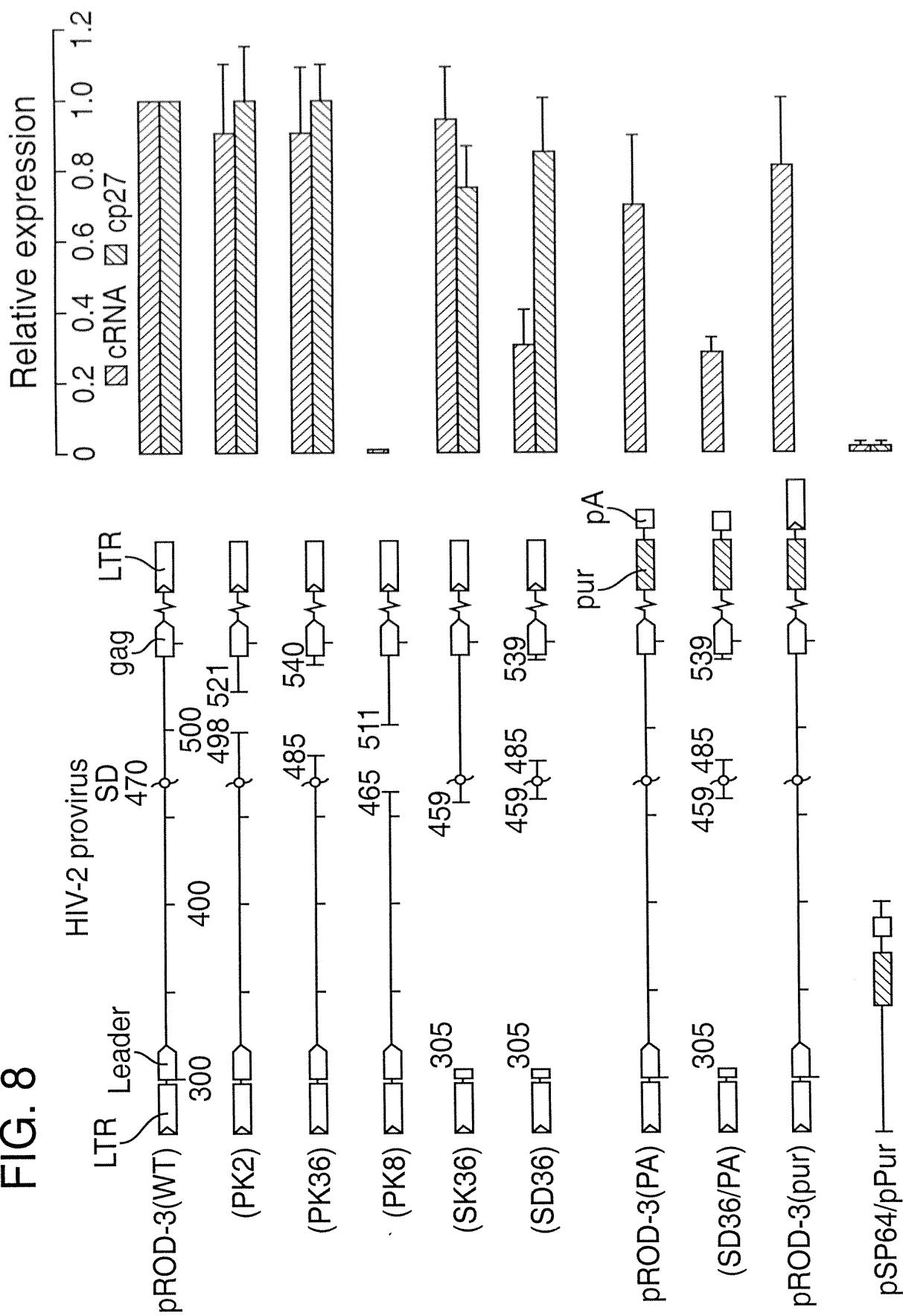


FIG. 9

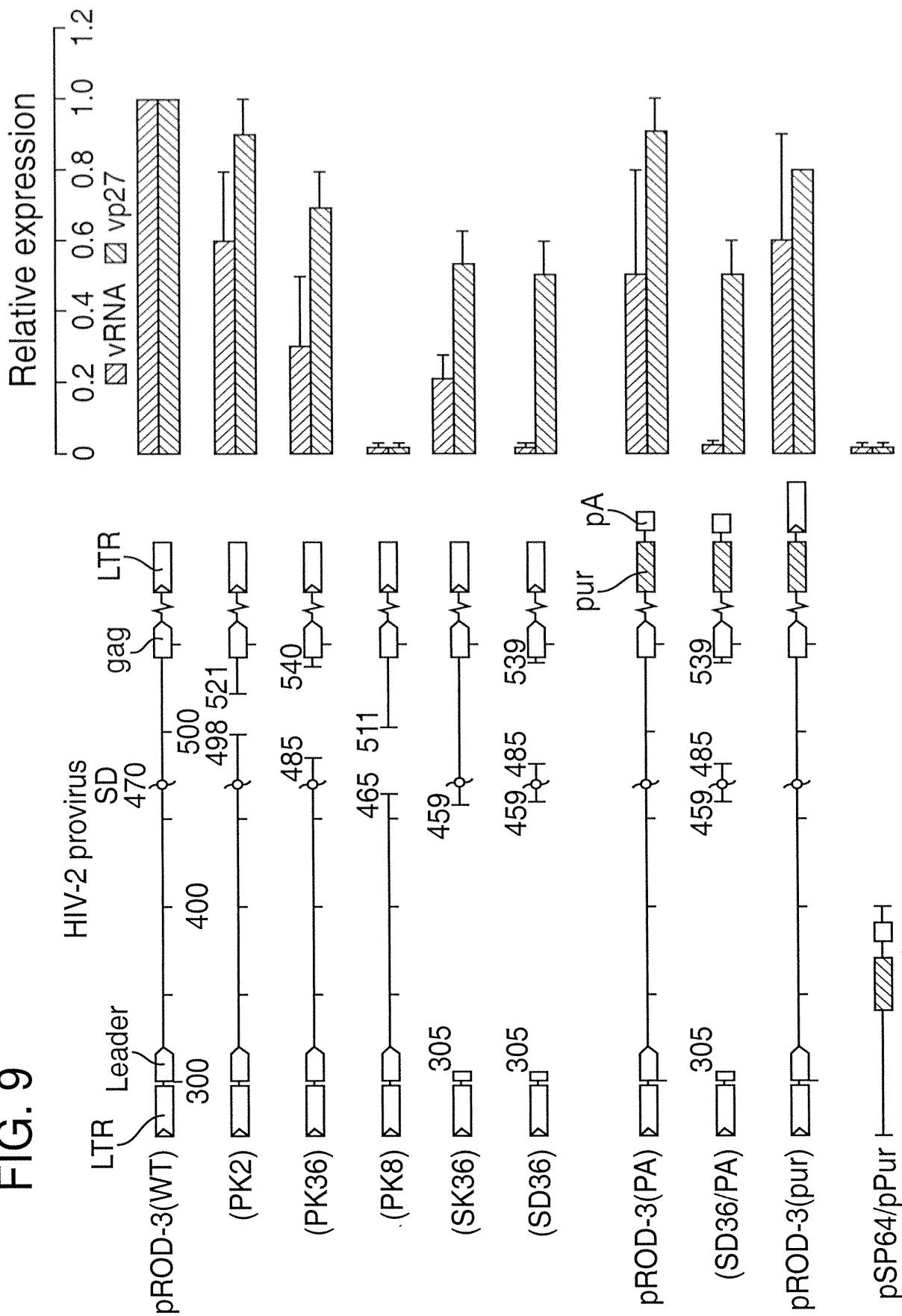


FIG. 10

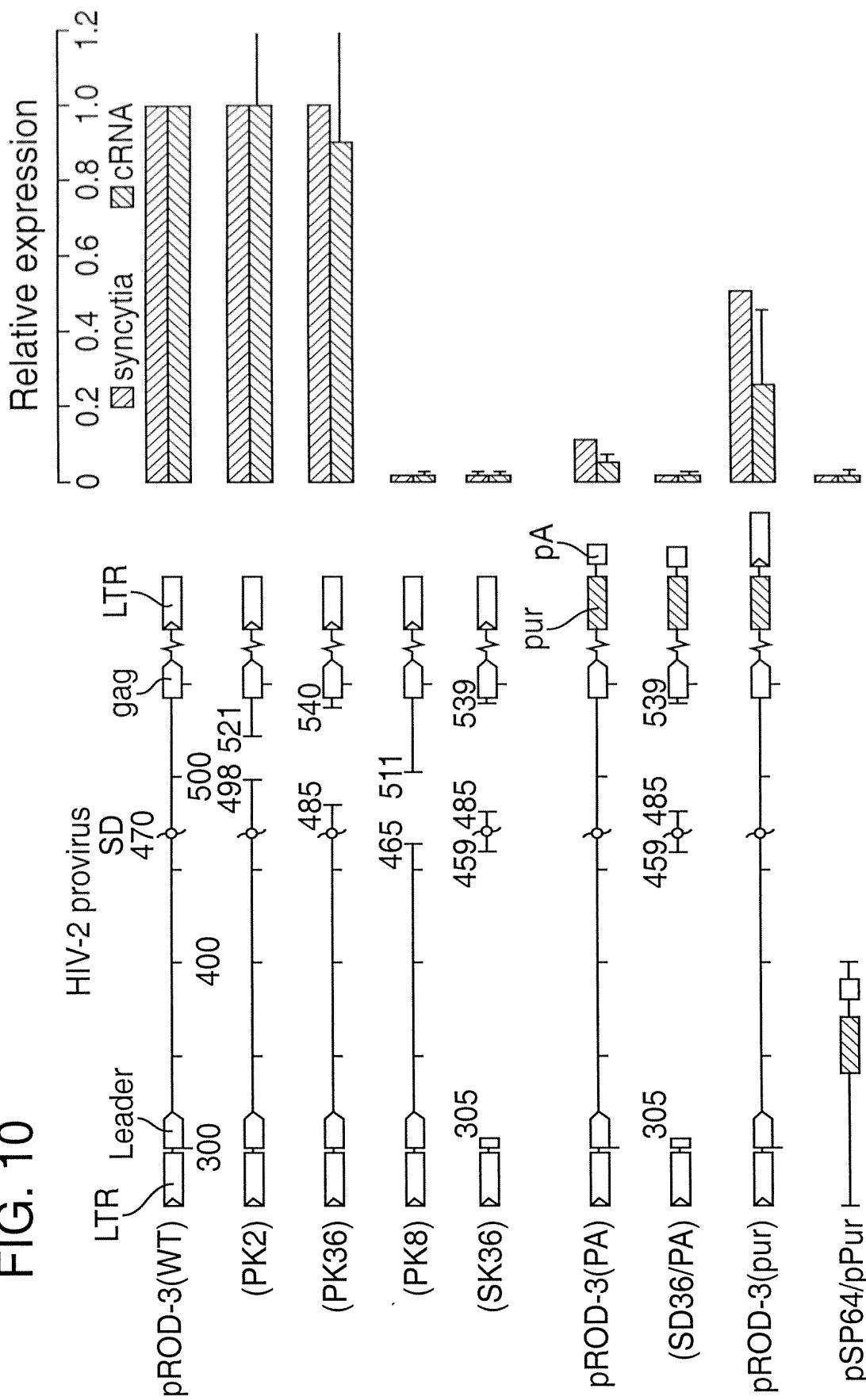


FIG. 11

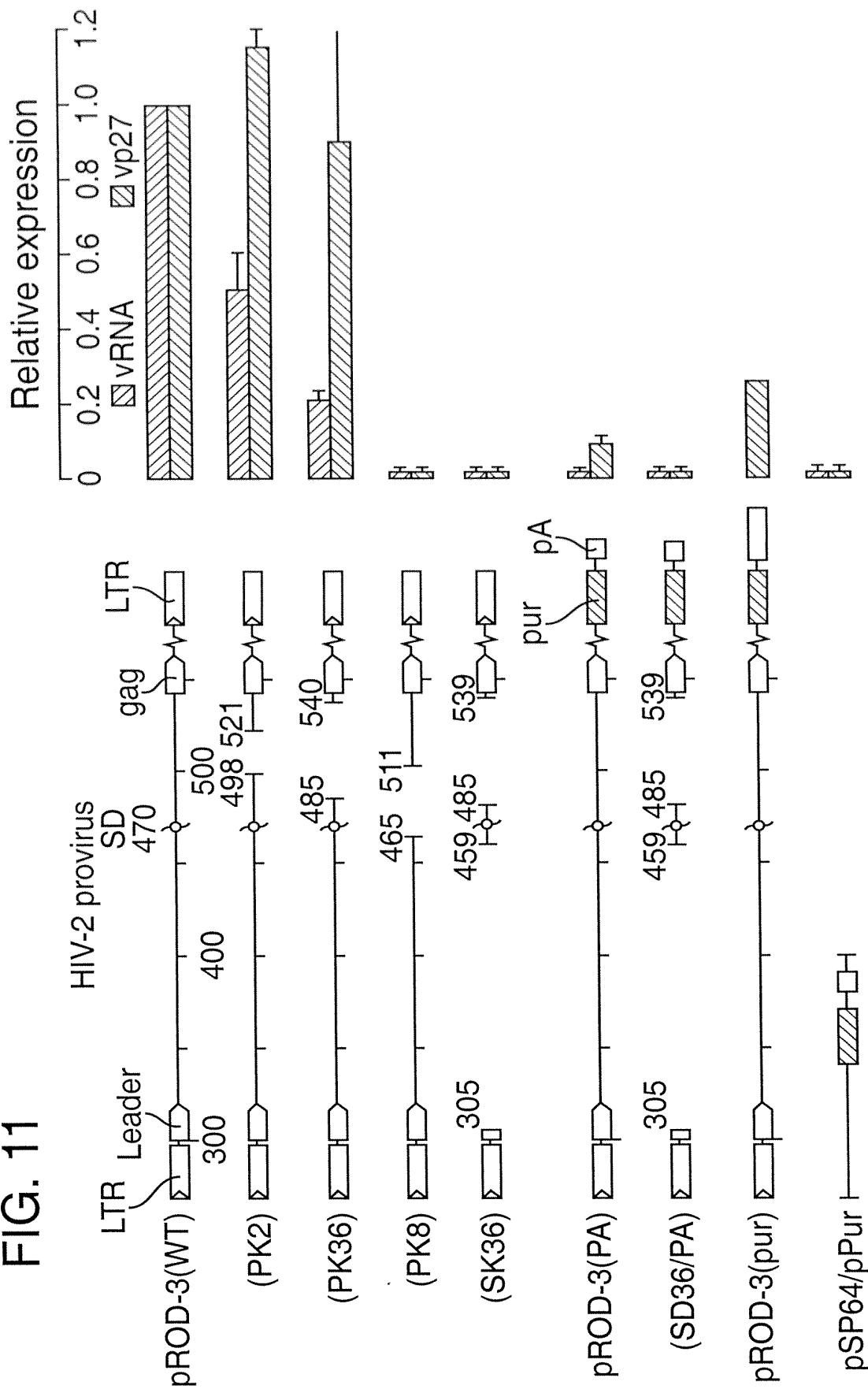


FIG. 14

HIV-2 Lentivirus: Gene Transfer Models

